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Accounting for Complex Population Structure in Pedigree and Genomic Analyses of Laying Chickens

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Cover Page Footnote

This project was supported by Hy-Line International.

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Accounting for Complex Population Structure in Pedigree and Genomic Analyses of Laying Chickens

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Summary and Implications

The objective of this study was to verify if fitting line composition in the model to analyze an admixed population would impact accuracy of pedigree and genomic estimated breeding values (EBV). Fitting line composition improved predictive ability for some traits in pedigree based analyses. In genomic prediction analyses, the accuracies for traits with high heritabilities were not affected by fitting line composition, whereas for lower heritability traits either positive or negative effects were observed. It was more important to correct for population structure in pedigree-based than in genomic analyses.

Introduction

In animal breeding programs, crossbreeding, admixture and introgression may be used to increase genetic variation in populations under selection. Joint pedigree-based analysis of such complex populations violates the assumption of individuals originating from a common base population and thus requires including genetic groups or otherwise fitting effects to account for line composition. Less is known about the impact of complex population structure on the accuracy of genomic breeding values, with some simulation studies (Toosi et al., 2010) suggesting that genomic models that fit markers simultaneously implicitly correct for population structure and no additional effects in the model are necessary. In this study we analyzed a chicken population with a history of line introgressions, using pedigree or genomic models, in order to determine the impact of fitting line composition on accuracy of estimated breeding values.

Materials and Methods

The study population included 3,537 birds from 7 generations genotyped with an Affymetrix 600K SNP panel or imputed from a 1K panel. After quality control, 171,938 segregating SNPs were retained. A total of 80,177 observations were included comprising individual performance or family means. Twenty six egg production and quality traits were analyzed. Accuracies of breeding value predictions were assessed as the correlation between EBV and hatch corrected phenotypes in 1,200 individuals from generation 8, which were genotyped with the 1K panel and imputed to 172k.

Results and Discussion

The Figure shows the distribution of changes in the accuracy of EBV after adding line composition in the model for the 26 traits, using either pedigree-based or genomic prediction.

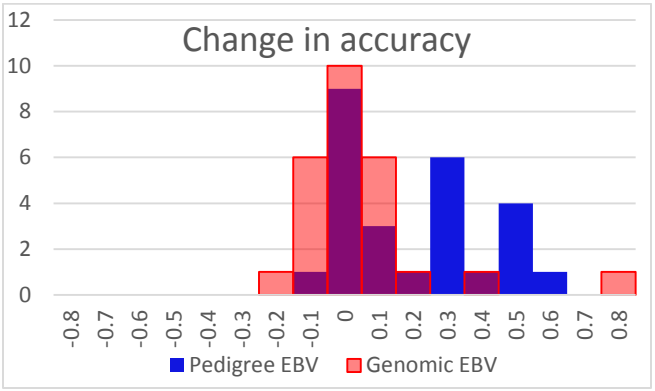

Figure. Distribution of the change in accuracy of EBV after including line composition in pedigree or genomic analyses

Fitting line composition in the model typically increased accuracy of pedigree-based EBVs more than for genomic EBVs (blue distribution is shifted to the right). The average changes were 0.16 and -0.01 for pedigree-based and genomic predictions, respectively. Genomic analysis may implicitly account for population structure when markers are fitted simultaneously.

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